C1 Figures 6A-6B summarize the experiments performed under various conditions for a Yeast Cell Cycle analysis.

Please replace the paragraph at page 21, lines 10 through 12 with the following paragraph:

C2 Yeast Experiments: Yeast data was downloaded from a Stanford University website. The 90 minute time point was excluded because of difficulties with scaling. See Figures 6A-B.

Please replace the paragraph at page 21, line 13 through page 22, line 6 with the following paragraph:

Expression Analysis: A detailed protocol can be found in Example 5. Briefly, 1 μg mRNA was used to generate first strand cDNA using a T7-linked oligo-dT primer. Following second strand synthesis, *in vitro* transcription (Ambion) was performed with biotinylated UTP and CTP (Enzo), resulting in 40-80 fold linear amplification of RNA. 40 μg of biotinylated RNA was fragmented to 50-150 nucleotide size prior to overnight hybridization to Affymetrix HU6000 arrays. Arrays contain probe sets for 6416 human genes (5223 known genes and 1193 ESTs). Because probe sets for some genes are present more than once on the array, the total number on the array is 7227. Following washing, arrays were stained with streptavidin-phycoerythrin (Molecular Probes) and scanned on a Hewlett-Packard scanner. Intensity values were scaled such that overall intensity for each chip of the same type was equivalent. Intensity for each feature of the array was captured using GeneChip software (Affymetrix, Inc.), and a single raw expression level for each gene was derived from the 20 probe pairs representing each gene using a trimmed mean algorithm. A threshold of 20 units was assigned to any gene with a calculated expression level below 20, since discrimination of expression below this level could not be performed with confidence.

Please replace the paragraph at page 24, lines 12 through 21 with the following paragraph:

C3 The myeloid leukemia cell line HL-60, which undergoes macrophage differentiation upon treatment with the phorbol ester TPA was studied. Nearly 100% of HL-60 cells become adherent

and exit the cell cycle within 24 hours of TPA treatment. To monitor this process at the transcriptional level, anti-sense cRNA was prepared from cells harvested at 0, 0.5, 4 and 24 hrs after TPA stimulation (see Example 1). Samples were then hybridized to expression-monitoring arrays from Affymetrix, Inc., containing oligonucleotide probes for 5223 known human genes and 1193 expressed sequence tags (ESTs), and hybridization intensities were determined for each gene.

Please replace the paragraph at page 27, lines 13 through 22 with the following paragraph:

The present invention was applied to more complex datasets involving multiple cell lines: HL-60 and the similar myeloid cell line U937, which also undergoes macrophage differentiation in response to TPA; Jurkat, a T-cell line that acquires many hallmarks of T-cell activation in response to TPA; and NB4, an acute promyelocytic leukemia cell line that undergoes neutrophilic differentiation in response to all-trans retinoic acid (ATRA). A total of 17 RNA samples were generated, yielding 6416 datapoints in 17-dimensional space. Of these, 1036 genes passed the variation filter. The genes were classified with a 6x4 SOM (Figure 5A-X), thereby grouping the 1036 genes into 24 categories.

Amendments to the specification are indicated in the attached "Marked Up Version of Amendments" (pages i - iii)

In the Claims

Please amend Claims 1 and 11. Amendments to the claims are indicated in the attached "Marked Up Version of Amendments" (page iv).

1. (Amended) In a computer system, a method for clustering a plurality of datapoints, wherein each datapoint is a series of gene expression values, wherein the method comprises:

a) receiving the gene expression values of the datapoints;